CLAIMS:

1. An array comprising a surface having attached thereto at least one cytosolic accessory protein free of it's membrane protein components or other subunits with which it is normally complexed.

2. An array as claimed in claim 1, wherein said cytosolic accessory proteins are cytosolic accessory proteins of membrane proteins which are members of a family of homologous membrane proteins

3. An array as claimed in claim 2, wherein the family of homologous membrane proteins is selected from the group consisting of ion-channels, G protein coupled receptors and transmembrane transporter poteins.

4. An array as claimed in claim 1, wherein said cytosolic accessory proteins are members of a family of homologous accessory proteins.

5. An array as claimed in claim 4, wherein said family is selected from the group consisting of ion-channel subunits, receptor interacting proteins and accessory proteins to membrane transporter proteins.

6. An array as claimed in claim 4 wherein said family is selected from the group consisting of K+-channel β-subunits, Ca2+-channel β-subunits, G protein subtypes and accessory proteins for transporters

7. An array as claimed in claim 4, wherein said family is selected from the group consisting of Kv channel β-subunits, Calcium channel β-subunits, G_s family, G_t family, G_i family, G_{i-0} family, G_{q-11} family, Gα-sensory family, βγ family and accessory proteins for transporters.

8. A method for determining which cytosolic accessory proteins interact with a given membrane protein, or vice versa, said method comprising the steps of:

(i) providing an array of candidate cytosolic accessory proteins free of their membrane protein components or other subunits with which they are normally complexed from one or more cytosolic accessory protein families of interest;

(ii) contacting the array with cytosolic fragments of said membrane protein and/or cytosolic fragments of other related membrane protein family members; and

(iii) detecting and identifying the interacting partners.

9. A method for screening compounds or peptides or proteins for the ability to interact selectively with a cytosolic accessory protein, said method comprising the steps of:

(i) providing an array of cytosolic accessory proteins free of their membrane protein components or other subunits with which they are normally complexed from one or more cytosolic protein families of interest;

(ii) contacting the array with compounds or peptides or proteins; and

(iii) identifying the interacting partners.

10. A method as claimed in claim 9, which method comprises the additional step (iv) of quantitating the interaction of the interacting partners.

11. A method for screening compounds or peptides or proteins for the ability to selectively modulate the interaction between a cytosolic accessory protein and a membrane protein, said method comprising the steps of

(i) providing an array of cytosolic accessory proteins free of their membrane protein components or other subunits with which they are normally complexed from one or more cytosolic protein families of interest;

(ii) contacting the array with compounds or peptides or proteins and with one or more membrane proteins or cytosolic fragments thereof of interest, either simultaneously or in sequence; and

(iii) determining whether said interaction is modulated by the presence of said compounds or peptides or proteins.

12. A method as claimed in claim 11, said method comprising the additional step (iv) of quantitating the degree of modulation of the interaction.

13. The use of an array of cytosolic accessory proteins as defined in any one of claims 1 to 7 to measure the relative catalytic activity of different members of a family of accessory proteins.

14. The use of an array of cytosolic accessory proteins as defined in any one of claims 1 to 7 as an affinity surface on which to select antibodies from a library of phenotype-genotype-linked antibodies (e.g. phage displayed antibodies).

15. The use of an array of cytosolic accessory proteins as defined in any one of claims 1 to 7 for determining the effect of post-translational modifications on the interactions of accessory proteins with membrane proteins and/or on the properties of said membrane proteins.